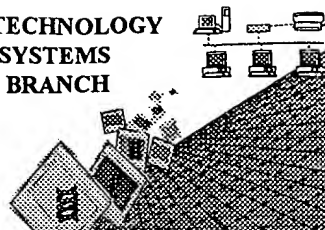BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/674,368 A_
Source: _PCT/09_
Date Processed by STIC: _2/6/2002_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
    U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
                Or
    U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _09/674,368A_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
   Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino
   Numbering

The numbering under each 5ᵗʰ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
   "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _2,4_____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences
   (OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences
   (NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's
   (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213>
   Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial-Sequence

11 _____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0
   "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/674,368A

DATE: 02/06/2002
TIME: 14:15:57

Does Not Comply
Corrected Diskette Needed

Input Set : A:\33377PCT.APP.txt
Output Set: N:\CRF3\02062002\I674368A.raw

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 5 <110> APPLICANT: American Cyanamid Company
 7 <120> TITLE OF INVENTION: Vaccines Containing Recombinant Pilin Against Neisseria
 9       Gonorrhoeae or Neisseria Meningitidis
11 <130> FILE REFERENCE: 33377-00/PCT
13 <140> CURRENT APPLICATION NUMBER: US/09/674,368A
14 <141> CURRENT FILING DATE: 2001-12-11
16 <160> NUMBER OF SEQ ID NOS: 24
18 <170> SOFTWARE: PatentIn Ver. 2.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 504
22 <212> TYPE: DNA
23 <213> ORGANISM: Artificial Sequence
25 <220> FEATURE:
26 <223> OTHER INFORMATION: Description of Artificial Sequence:Chimeric of
27       Neisseria Meningitidis Class I and Neisseria
28       Gonorrhoeae
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)..(501)
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38  1               5                  10                  15
40 atc gcc atc gtc ggc att ttg gcg gca gtc gcc ctt ccc gcc tac caa 96
41 Ile Ala Ile Val Gly Ile Leu Ala Ala Val Ala Leu Pro Ala Tyr Gln
42             20                  25                  30
44 gac tac acc gcc cgc gcg caa gtt tcc gaa gcc atc ctt ttg gcc gaa 144
45 Asp Tyr Thr Ala Arg Ala Gln Val Ser Glu Ala Ile Leu Leu Ala Glu
46         35                  40                  45
48 ggt caa aaa tca gcc gtt acc gag tat tac ctg aat cac ggc gaa tgg 192
49 Gly Gln Lys Ser Ala Val Thr Glu Tyr Tyr Leu Asn His Gly Glu Trp
50     50                  55                  60
52 ccc ggc aac aac act tct gcc ggc gtg gca tct tct tca aca atc aaa 240
53 Pro Gly Asn Asn Thr Ser Ala Gly Val Ala Ser Ser Ser Thr Ile Lys
54 65                  70                  75                  80
58 ggc aaa tat gtt aag gaa gtt aca gtc gca aac ggc gtc att acc gcc 288
59 Gly Lys Tyr Val Lys Glu Val Thr Val Ala Asn Gly Val Ile Thr Ala
60          85              85              90      90      95      95
62 aca atg ctt tca agc ggc gta aac aaa gaa atc caa ggc aaa aaa ctc 336
63 Thr Met Leu Ser Ser Gly Val Asn Lys Glu Ile Gln Gly Lys Lys Leu
64             100                 105                 110
66 tcc ctg tgg gcc aag cgt caa gac ggt tcg gta aaa tgg ttc tgc gga 384
67 Ser Leu Trp Ala Lys Arg Gln Asp Gly Ser Val Lys Trp Phe Cys Gly
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W--> (←— fix numbering)

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RAW SEQUENCE LISTING                    DATE: 02/06/2002
PATENT APPLICATION:  US/09/674,368A     TIME: 14:15:57

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        Output Set: N:\CRF3\02062002\I674368A.raw

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     70 cag ccg gtt acg cgc acc gac gcc aaa gcc gac acc gtc gcc gcc gcc 432
     71 Gln Pro Val Thr Arg Thr Asp Ala Lys Ala Asp Thr Val Ala Ala Ala
     72           130                    135                    140        .
     74 gcc aag acc gcc gac aac atc aac acc aag cac ctg ccg tca acc tgc    480
     75 Ala Lys Thr Ala Asp Asn Ile Asn Thr Lys His Leu Pro Ser Thr Cys
W--> 76 145                    150                    155                    160
     78 cgc gac gca agt gat gcc agc taa                          ,        504
     79 Arg Asp Ala Ser Asp Ala Ser
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     83 <211> LENGTH: 167
     84 <212> TYPE: PRT
     85 <213> ORGANISM: Artificial Sequence        see item 6 on Erra Summary Sheet
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     91 Ile Ala Ile Val Gly Ile Leu Ala Ala Val Ala Leu Pro Ala Tyr Gln
     92           20                    25                   30
     95 Asp Tyr Thr Ala Arg Ala Gln Val Ser Glu Ala Ile Leu Leu Ala Glu
     96           35                    40                   45
     99 Gly Gln Lys Ser Ala Val Thr Glu Tyr Tyr Leu Asn His Gly Glu Trp
    100      50                    55                   60
    103 Pro Gly Asn Asn Thr Ser Ala Gly Val Ala Ser Ser Ser Thr Ile Lys
    104 65                    70                   75                   80
    107 Gly Lys Tyr Val Lys Glu Val Thr Val Ala Asn Gly Val Ile Thr Ala
    108           85                    90                   95
    111 Thr Met Leu Ser Ser Gly Val Asn Lys Glu Ile Gln Gly Lys Lys Leu
    112           100                   105                  110
    115 Ser Leu Trp Ala Lys Arg Gln Asp Gly Ser Val Lys Trp Phe Cys Gly
    116           115                   120                  125
    118 Gln Pro Val Thr Arg Thr Asp Ala Lys Ala Asp Thr Val Ala Ala Ala
    119      130                    135                  140
    121 Ala Lys Thr Ala Asp Asn Ile Asn Thr Lys His Leu Pro Ser Thr Cys
    122 145                   150                    155                  160
    124 Arg Asp Ala Ser Asp Ala Ser
    125                     165   .
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    131 <213> ORGANISM: Artificial Sequence
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    135       Neisseria Meningitidis Class II and Neisseria
    136       Gonorrhoeae
    138 <220> FEATURE:
    139 <221> NAME/KEY: CDS
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145  1               5                  10                  15
147 atc gcc atc gtc ggt atc ttg gca gcc gtc gcc ctg ccc gca tac caa    96
148 Ile Ala Ile Val Gly Ile Leu Ala Ala Val Ala Leu Pro Ala Tyr Gln
149                 20                  25                  30
151 gac tac acc gcg cgc gcc caa atg tcc gaa gcc ctg act ttg gca gaa   144
152 Asp Tyr Thr Ala Arg Ala Gln Met Ser Glu Ala Leu Thr Leu Ala Glu
153             35                  40                  45
155 ggt caa aaa tcc gca gtg atc gag tat tat tcc gac aac ggc aca ttc   192
156 Gly Gln Lys Ser Ala Val Ile Glu Tyr Tyr Ser Asp Asn Gly Thr Phe
157     50                  55                  60
159 ccg aac agc aat act tcc gca ggt att gct gcc tct aac gag att aaa   240
160 Pro Asn Ser Asn Thr Ser Ala Gly Ile Ala Ala Ser Asn Glu Ile Lys
161  65                  70                  75                  80
163 ggt aag tat gtg gca tcg gtt aag gtt gaa ggt aat gcc tct gtt gct   288
164 Gly Lys Tyr Val Ala Ser Val Lys Val Glu Gly Asn Ala Ser Val Ala
165                 85                  90                  95
167 tct att acc gct acc atg aac tct agt aat gtg aat aag gac atc aaa   336
168 Ser Ile Thr Ala Thr Met Asn Ser Ser Asn Val Asn Lys Asp Ile Lys
169             100                 105                 110
172 ggt aaa acc ttg gta ctc gtc ggc aaa caa aac tcc ggt tcg gta aaa   384
173 Gly Lys Thr Leu Val Leu Val Gly Lys Gln Asn Ser Gly Ser Val Lys
174         115                 120                 125
176 tgg ttc tgc gga cag ccg gtt acg cgc gac aac gcc gac aac gac gac   432
177 Trp Phe Cys Gly Gln Pro Val Thr Arg Asp Asn Ala Asp Asn Asp Asp
178     130                 135                 140
180 gtc aaa gac gcc ggc aac aac ggc atc gaa acc aag cac ctg ccg tca   480
181 Val Lys Asp Ala Gly Asn Asn Gly Ile Glu Thr Lys His Leu Pro Ser
182 145                 150                 155                 160
184 acc tgc cgc gat acg tca tct gat gcc aaa                           510
185 Thr Cys Arg Asp Thr Ser Ser Asp Ala Lys
186                 165                 170
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196  1               5                  10                  15
198 Ile Ala Ile Val Gly Ile Leu Ala Ala Val Ala Leu Pro Ala Tyr Gln
199                 20                  25                  30
201 Asp Tyr Thr Ala Arg Ala Gln Met Ser Glu Ala Leu Thr Leu Ala Glu
202             35                  40                  45
204 Gly Gln Lys Ser Ala Val Ile Glu Tyr Tyr Ser Asp Asn Gly Thr Phe
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W-->
W-->

item 6

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205      50                    55                    60
207 Pro Asn Ser Asn Thr Ser Ala Gly Ile Ala Ala Ser Asn Glu Ile Lys
208  65        .              70                75                80
210 Gly Lys Tyr Val Ala Ser Val Lys Val Glu Gly Asn Ala Ser Val Ala
211                  85                90                95
213 Ser Ile Thr Ala Thr Met Asn Ser Ser Asn Val Asn Lys Asp Ile Lys
214                100              105              110
216 Gly Lys Thr Leu Val Leu Val Gly Lys Gln Asn Ser Gly Ser Val Lys
217          115              120                    125
219 Trp Phe Cys Gly Gln Pro Val Thr Arg Asp Asn Ala Asp Asn Asp Asp
220      130              135                140
222 Val Lys Asp Ala Gly Asn Asn Gly Ile Glu Thr Lys His Leu Pro Ser
223 145              150                155        .        160
225 Thr Cys Arg Asp Thr Ser Ser Asp Ala Lys
226                165                170
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233 <213> ORGANISM: Neisseria gonorrhoeae
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267 <213> ORGANISM: Neisseria gonorrhoeae
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273 <211> LENGTH: 28
274 <212> TYPE: DNA
275 <213> ORGANISM: Neisseria gonorrhoeae
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293 <213> ORGANISM: Neisseria Meningitidis Class I
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VERIFICATION SUMMARY   DATE: 02/06/2002
PATENT APPLICATION: US/09/674,368A   TIME: 14:15:59

Input Set : A:\33377PCT.APP.txt
Output Set: N:\CRF3\02062002\I674368A.raw

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L:13 M:270 C: Current Application Number differs, Replaced Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:60 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:64 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:68 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:72 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
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